SEQUENCE LISTING

<110> Feder, J. N.
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<120> A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY6,
EXPRESSED HIGHLY IN SMALL INTESTINE

<130> D0040NP/3053-4119US3

<140> TBA
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<150> 60/235,602
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<150> 60/306,604
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<150> 60/315,412
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35 40 45

Val Ser Ser Ser Thr Phe Ile His Thr Asn Val Asp Gly Leu Asn Pro
50 55 60

Asp Ala Gln Thr Glu Leu Gln Val Leu Leu Asn Met Thr Lys Asn Tyr
65 70 75 80

Thr Lys Thr Cys Gly Phe Val Val Tyr Gln Asn Asp Lys Leu Phe Gln
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Cys Gln Lys Asp Lys Gly Thr Asp Gly Phe Leu Arg Cys Arg Cys Asn
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His Thr Thr Asn Phe Ala Val Leu Met Thr Phe Lys Lys Asp Tyr Gln
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Tyr Pro Lys Ser Leu Asp Ile Leu Ser Asn Val Gly Cys Ala Leu Ser
        195                 200                 205

Val Thr Gly Leu Ala Leu Thr Val Ile Phe Gln Ile Val Thr Arg Lys
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Val Arg Lys Thr Ser Val Thr Trp Val Leu Val Asn Leu Cys Ile Ser
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Thr Met Lys Pro Leu Pro Arg His Phe Ile Leu Phe Ile Ser Leu Ile
                325                 330                 335

Gly Trp Gly Val Pro Ala Ile Val Val Ala Ile Thr Val Gly Val Ile
            340                 345                 350

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420 425 430

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Leu Ala Tyr Leu Met Leu Val Asn Asp Asp Ser Ile Arg Ile Val Phe
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Ser Tyr Ile Phe Cys Leu Phe Asn Thr Thr Gln Gly Leu Gln Ile Phe
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Ile Leu Tyr Thr Val Arg Thr Lys Val Phe Gln Ser Glu Ala Ser Lys
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Val Leu Met Leu Leu Ser Ser Ile Gly Arg Arg Lys Ser Leu Pro Ser
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Val Thr Arg Pro Arg Leu Arg Val Lys Met Tyr Asn Phe Leu Arg Ser
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ttgttcctta tatcgttaaa tctttgtgac acactttgac aaaaatgtag aacctataac 300
aaattctttt acaagttact ataaaggaca caaagagaaa actttacctt ccagaacaaa 360
atgactcctg atgaacagtg tgtggggatt tgcttgtatg tattaaactt ttgacctctg 420
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35 40 45

Asp Val Ile Met Ile Glu Ser Ala Asn Tyr Gly Arg Thr Asp Asp Lys
50 55 60

Ile Cys Asp Ser Asp Pro Ala Gln Met Glu Asn Ile Arg Cys Tyr Leu
65 70 75 80

Pro Asp Ala Tyr Lys Ile Met Ser Gln Arg Cys Asn Asn Arg Thr Gln
85 90 95

Cys Ala Val Val Ala Gly Pro Asp Val Phe Pro Asp Pro Cys Pro Gly
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Thr Tyr Lys Tyr Leu Glu Val Gln Tyr Glu Cys Val Pro Tyr Lys Val
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Glu Gln Lys Val Phe Leu Cys Pro Gly Leu Leu Lys Gly Val Tyr Gln
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Ser Glu His Leu Phe Glu Ser Asp His Gln Ser Gly Ala Trp Cys Lys
145 150 155 160

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165 170 175

Tyr Arg Thr Asp Thr Leu Thr Glu Tyr Ser Ser Lys Asp Asp Phe Ile
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195 200 205

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Thr Arg Asn Ile Val Lys Phe Asp Leu Arg Thr Arg Ile Lys Ser Gly
225 230 235 240

Glu Ala Ile Ile Ala Asn Ala Asn Tyr His Asp Thr Ser Pro Tyr Arg
245 250 255

Trp Gly Gly Lys Ser Asp Ile Asp Leu Ala Val Asp Glu Asn Gly Leu
260 265 270

Trp Val Ile Tyr Ala Thr Glu Gln Asn Asn Gly Lys Ile Val Ile Ser
275 280 285

Gln Leu Asn Pro Tyr Thr Leu Arg Ile Glu Gly Thr Trp Asp Thr Ala
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Tyr Asp Lys Arg Ser Ala Ser Asn Ala Phe Met Ile Cys Gly Ile Leu
305 310 315 320

Tyr Val Val Lys Ser Val Tyr Glu Asp Asp Asp Asn Glu Ala Thr Gly
325 330 335

Asn Lys Ile Asp Tyr Ile Tyr Asn Thr Asp Gln Ser Lys Asp Ser Leu
340 345 350

Val Asp Val Pro Phe Pro Asn Ser Tyr Gln Tyr Ile Ala Ala Val Asp
355 360 365

Tyr Asn Pro Arg Asp Asn Leu Leu Tyr Val Trp Asn Asn Tyr His Val
370 375 380

Val Lys Tyr Ser Leu Asp Phe Gly Pro Leu Asp Ser Arg Ser Gly Pro
385 390 395 400

Val His His Gly Gln Val Ser Tyr Ile Ser Pro Pro Ile His Leu Asp
405 410 415

Ser Asp Leu Glu Arg Pro Pro Val Arg Gly Ile Ser Thr Thr Gly Pro
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Leu Gly Met Gly Ser Thr Thr Thr Ser Thr Thr Leu Arg Thr Thr Thr
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Trp Asn Leu Gly Arg Ser Thr Thr Pro Ser Leu Pro Gly Arg Arg Asn
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Arg Ser Thr Ser Thr Pro Ser Pro Ala Ile Glu Val Leu Asp Val Thr
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485 490 495

Cys Glu Ala Val Glu Ala Arg Glu Ile Met Trp Phe Lys Thr Arg Gln
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Gly Gln Val Ala Lys Gln Ser Cys Pro Ala Gly Thr Ile Gly Val Ser
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Thr Tyr Leu Cys Leu Ala Pro Asp Gly Ile Trp Asp Pro Gln Gly Pro
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Asp Leu Ser Asn Cys Ser Ser Pro Trp Val Asn His Ile Thr Gln Lys
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Leu Lys Ser Gly Glu Thr Ala Ala Asn Ile Ala Arg Glu Leu Ala Glu
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Gln Thr Arg Asn His Leu Asn Ala Gly Asp Ile Thr Tyr Ser Val Arg
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Ala Met Asp Gln Leu Val Gly Leu Leu Asp Val Gln Leu Arg Asn Leu
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Thr Pro Gly Gly Lys Asp Ser Ala Ala Arg Ser Leu Asn Lys Leu Gln
610 615 620

Lys Arg Glu Arg Ser Cys Arg Ala Tyr Val Gln Ala Met Val Glu Thr
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Val Asn Asn Leu Leu Gln Pro Gln Ala Leu Asn Ala Trp Arg Asp Leu
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Thr Thr Ser Asp Gln Leu Arg Ala Ala Thr Met Leu Leu Asp Thr Val
660 665 670

Glu Glu Ser Ala Phe Val Leu Ala Asp Asn Leu Leu Lys Thr Asp Ile
675 680 685

Val Arg Glu Asn Thr Asp Asn Ile Gln Leu Glu Val Ala Arg Leu Ser
690 695 700

Thr Glu Gly Asn Leu Glu Asp Leu Lys Phe Pro Glu Asn Thr Gly His
705 710 715 720

Gly Ser Thr Ile Gln Leu Ser Ala Asn Thr Leu Lys Gln Asn Gly Arg
725 730 735

Asn Gly Glu Ile Arg Val Ala Phe Val Leu Tyr Asn Asn Leu Gly Pro
740 745 750

Tyr Leu Ser Thr Glu Asn Ala Ser Met Lys Leu Gly Thr Glu Ala Met
755 760 765

Ser Thr Asn His Ser Val Ile Val Asn Ser Pro Val Ile Thr Ala Ala
770 775 780

Ile Asn Lys Glu Phe Ser Asn Lys Val Tyr Leu Ala Asp Pro Val Val
785 790 795 800

Phe Thr Val Lys His Ile Lys Gln Ser Glu Glu Asn Phe Asn Pro Asn
805 810 815

Cys Ser Phe Trp Ser Tyr Ser Lys Arg Thr Met Thr Gly Tyr Trp Ser
820 825 830

Thr Gln Gly Cys Arg Leu Leu Thr Thr Asn Lys Thr His Thr Thr Cys
835 840 845

Ser Cys Asn His Leu Thr Asn Phe Ala Val Leu Met Ala His Val Glu
850 855 860

Val Lys His Ser Asp Ala Val His Asp Leu Leu Leu Asp Val Ile Thr
865 870 875 880

Trp Val Gly Ile Leu Leu Ser Leu Val Cys Leu Leu Ile Cys Ile Phe
885 890 895

Thr Phe Cys Phe Phe Arg Gly Leu Gln Ser Asp Arg Asn Thr Ile His
900 905 910

Lys Asn Leu Cys Ile Ser Leu Phe Val Ala Glu Leu Leu Phe Leu Ile
915 920 925

Gly Ile Asn Arg Thr Asp Gln Pro Ile Ala Cys Ala Val Phe Ala Ala
930 935 940

Leu Leu His Phe Phe Phe Leu Ala Ala Phe Thr Trp Met Phe Leu Glu
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Gly Val Gln Leu Tyr Ile Met Leu Val Glu Val Phe Glu Ser Glu His
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Ser Arg Arg Lys Tyr Phe Tyr Leu Val Gly Tyr Gly Met Pro Ala Leu
980 985 990

Ile Val Ala Val Ser Ala Ala Val Asp Tyr Arg Ser Tyr Gly Thr Asp
995 1000 1005

Lys Val Cys Trp Leu Arg Leu Asp Thr Tyr Phe Ile Trp Ser Phe Ile
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Gly Pro Ala Thr Leu Ile Ile Met Leu Asn Val Ile Phe Leu Gly Ile
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Ala Leu Tyr Lys Met Phe His His Thr Ala Ile Leu Lys Pro Glu Ser
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Gly Cys Leu Asp Asn Ile Lys Ser Trp Val Ile Gly Ala Ile Ala Leu
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Leu Cys Leu Leu Gly Leu Thr Trp Ala Phe Gly Leu Met Tyr Ile Asn
1075 1080 1085

Glu Ser Thr Val Ile Met Ala Tyr Leu Phe Thr Ile Phe Asn Ser Leu
1090 1095 1100

Gln Gly Met Phe Ile Phe Ile Phe His Cys Val Leu Gln Lys Lys Val
1105 1110 1115 1120

Arg Lys Glu Tyr Gly Lys Cys Leu Arg Thr His Cys Cys Ser Gly Lys
1125 1130 1135

Ser Thr Glu Ser Ser Ile Gly Ser Gly Lys Thr Ser Gly Ser Arg Thr
1140 1145 1150

Pro Gly Arg Tyr Ser Thr Gly Ser Gln Ser Arg Ile Arg Arg Met Trp
1155 1160 1165

Asn Asp Thr Val Arg Lys Gln Ser Glu Ser Ser Phe Ile Thr Gly Asp
1170 1175 1180

Ile Asn Ser Ser Ala Ser Leu Asn Arg Glu Pro Tyr Arg Glu Thr Ser
1185 1190 1195 1200

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Leu Arg His Ala Glu His Ser Pro Gly Gly Pro Leu Pro Pro Arg His
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Leu Leu Gln Gln Pro Ala Ala Glu Arg Ser Thr Ala His Arg Gly Gln
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Gly Pro Arg Gly Thr Ala Arg Gly Val Arg Gly Pro Gly Ala Pro Gly
65   70   75   80

Ala Gln Ile Ala Ala Gln Ala Phe Ser Arg Ala Pro Ile Pro Met Ala
                85   90   95

Val Val Arg Arg Glu Leu Ser Cys Glu Ser Tyr Pro Ile Glu Leu Arg
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Cys Pro Gly Thr Asp Val Ile Met Ile Glu Ser Ala Asn Tyr Gly Arg
        115   120   125

Thr Asp Asp Lys Ile Cys Asp Ser Asp Pro Ala Gln Met Glu Asn Ile
    130   135   140

Arg Cys Tyr Leu Pro Asp Ala Tyr Lys Ile Met Ser Gln Arg Cys Asn
145   150   155   160

Asn Arg Thr Gln Cys Ala Val Val Ala Gly Pro Asp Val Phe Pro Asp
                165   170   175

Pro Cys Pro Gly Thr Tyr Lys Tyr Leu Glu Val Gln Tyr Glu Cys Val
            180   185   190

Pro Tyr Lys Val Glu Gln Lys Val Phe Leu Cys Pro Gly Leu Leu Lys
        195   200   205

Gly Val Tyr Gln Ser Glu His Leu Phe Glu Ser Asp His Gln Ser Gly
    210   215   220

Ala Trp Cys Lys Asp Pro Leu Gln Ala Ser Asp Lys Ile Tyr Tyr Met
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Pro Trp Thr Pro Tyr Arg Thr Asp Thr Leu Thr Glu Tyr Ser Ser Lys

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305                 310                 315                 320

Ser Pro Tyr Arg Trp Gly Gly Lys Ser Asp Ile Asp Leu Ala Val Asp
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            340                 345                 350

Ile Val Ile Ser Gln Leu Asn Pro Tyr Thr Leu Arg Ile Glu Gly Thr
        355                 360                 365

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Glu Ala Thr Gly Asn Lys Ile Asp Tyr Ile Tyr Asn Thr Asp Gln Ser
                405                 410                 415

Lys Asp Ser Leu Val Asp Val Pro Phe Pro Asn Ser Tyr Gln Tyr Ile
            420                 425                 430

Ala Ala Val Asp Tyr Asn Pro Arg Asp Asn Leu Leu Tyr Val Trp Asn
        435                 440                 445

Asn Tyr His Val Val Lys Tyr Ser Leu Asp Phe Gly Pro Leu Asp Ser
    450                 455                 460

Arg Ser Gly Pro Val His His Gly Gln Val Ser Tyr Ile Ser Pro Pro
465                 470                 475                 480

Ile His Leu Asp Ser Asp Leu Glu Arg Pro Pro Val Arg Gly Ile Ser
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Thr Thr Gly Pro Leu Gly Met Gly Ser Thr Thr Thr Ser Thr Thr Leu
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Leu Asp Val Thr Thr His Leu Pro Ser Ala Ala Ser Gln Ile Pro Ala
545                 550                 555                 560

Met Glu Glu Ser Cys Glu Ala Val Glu Ala Arg Glu Ile Met Trp Phe
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Lys Thr Arg Gln Gly Gln Val Ala Lys Gln Ser Cys Pro Ala Gly Thr
            580                 585                 590

Ile Gly Val Ser Thr Tyr Leu Cys Leu Ala Pro Asp Gly Ile Trp Asp
        595                 600                 605

Pro Gln Gly Pro Asp Leu Ser Asn Cys Ser Ser Pro Trp Val Asn His
    610                 615                 620

Ile Thr Gln Lys Leu Lys Ser Gly Glu Thr Ala Ala Asn Ile Ala Arg
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Glu Leu Ala Glu Gln Thr Arg Asn His Leu Asn Ala Gly Asp Ile Thr
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Tyr Ser Val Arg Ala Met Asp Gln Leu Val Gly Leu Leu Asp Val Gln
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Leu Arg Asn Leu Thr Pro Gly Gly Lys Asp Ser Ala Ala Arg Ser Leu
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Asn Lys Leu Gln Lys Arg Glu Arg Ser Cys Arg Ala Tyr Val Gln Ala
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Met Val Glu Thr Val Asn Asn Leu Leu Gln Pro Gln Ala Leu Asn Ala
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Trp Arg Asp Leu Thr Thr Ser Asp Gln Leu Arg Ala Ala Thr Met Leu
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Leu Asp Thr Val Glu Glu Ser Ala Phe Val Leu Ala Asp Asn Leu Leu
            740                 745                 750

Lys Thr Asp Ile Val Arg Glu Asn Thr Asp Asn Ile Gln Leu Glu Val
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Ala Arg Leu Ser Thr Glu Gly Asn Leu Glu Asp Leu Lys Phe Pro Glu
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785                 790                 795                 800

Gln Asn Gly Arg Asn Gly Glu Ile Arg Val Ala Phe Val Leu Tyr Asn
                805                 810                 815

Asn Leu Gly Pro Tyr Leu Ser Thr Glu Asn Ala Ser Met Lys Leu Gly
            820                 825                 830

Thr Glu Ala Met Ser Thr Asn His Ser Val Ile Val Asn Ser Pro Val
        835                 840                 845

Ile Thr Ala Ala Ile Asn Lys Glu Phe Ser Asn Lys Val Tyr Leu Ala
    850                 855                 860

Asp Pro Val Val Phe Thr Val Lys His Ile Lys Gln Ser Glu Glu Asn
865                 870                 875                 880

Phe Asn Pro Asn Cys Ser Phe Trp Ser Tyr Ser Lys Arg Thr Met Thr
                885                 890                 895

Gly Tyr Trp Ser Thr Gln Gly Cys Arg Leu Leu Thr Thr Asn Lys Thr
            900                 905                 910

His Thr Thr Cys Ser Cys Asn His Leu Thr Asn Phe Ala Val Leu Met
        915                 920                 925

Ala His Val Glu Val Lys His Ser Asp Ala Val His Asp Leu Leu Leu
    930                 935                 940

Asp Val Ile Thr Trp Val Gly Ile Leu Leu Ser Leu Val Cys Leu Leu
945                 950                 955                 960

Ile Cys Ile Phe Thr Phe Cys Phe Phe Arg Gly Leu Gln Ser Asp Arg
                965                 970                 975

Asn Thr Ile His Lys Asn Leu Cys Ile Ser Leu Phe Val Ala Glu Leu
            980                 985                 990

Leu Phe Leu Ile Gly Ile Asn Arg Thr Asp Gln Pro Ile Ala Cys Ala
        995                1000                1005

Val Phe Ala Ala Leu Leu His Phe Phe Phe Leu Ala Ala Phe Thr Trp
```

```
   1010                1015                1020

Met Phe Leu Glu Gly Val Gln Leu Tyr Ile Met Leu Val Glu Val Phe
1025                1030                1035                1040

Glu Ser Glu His Ser Arg Arg Lys Tyr Phe Tyr Leu Val Gly Tyr Gly
                1045                1050                1055

Met Pro Ala Leu Ile Val Ala Val Ser Ala Ala Val Asp Tyr Arg Ser
            1060                1065                1070

Tyr Gly Thr Asp Lys Val Cys Trp Leu Arg Leu Asp Thr Tyr Phe Ile
        1075                1080                1085

Trp Ser Phe Ile Gly Pro Ala Thr Leu Ile Ile Met Leu Asn Val Ile
    1090                1095                1100

Phe Leu Gly Ile Ala Leu Tyr Lys Met Phe His His Thr Ala Ile Leu
1105                1110                1115                1120

Lys Pro Glu Ser Gly Cys Leu Asp Asn Ile Lys Ser Trp Val Ile Gly
                1125                1130                1135

Ala Ile Ala Leu Leu Cys Leu Leu Gly Leu Thr Trp Ala Phe Gly Leu
            1140                1145                1150

Met Tyr Ile Asn Glu Ser Thr Val Ile Met Ala Tyr Leu Phe Thr Ile
        1155                1160                1165

Phe Asn Ser Leu Gln Gly Met Phe Ile Phe Ile Phe His Cys Val Leu
    1170                1175                1180

Gln Lys Lys Val Arg Lys Glu Tyr Gly Lys Cys Leu Arg Thr His Cys
1185                1190                1195                1200

Cys Ser Gly Lys Ser Thr Glu Ser Ser Ile Gly Ser Gly Lys Thr Ser
                1205                1210                1215

Gly Ser Arg Thr Pro Gly Arg Tyr Ser Thr Gly Ser Gln Ser Arg Ile
            1220                1225                1230

Arg Arg Met Trp Asn Asp Thr Val Arg Lys Gln Ser Glu Ser Ser Phe
        1235                1240                1245

Ile Thr Gly Asp Ile Asn Ser Ser Ala Ser Leu Asn Arg Glu Gly Leu
    1250                1255                1260

Leu Asn Asn Ala Arg Asp Thr Ser Val Met Asp Thr Leu Pro Leu Asn
```

1265 1270 1275 1280

Gly Asn His Gly Asn Ser Tyr Ser Ile Ala Gly Gly Glu Tyr Leu Ser
1285 1290 1295

Asn Cys Val Gln Ile Ile Asp Arg Gly Tyr Asn His Asn Glu Thr Ala
1300 1305 1310

Leu Glu Lys Lys Ile Leu Lys Glu Leu Thr Ser Asn Tyr Ile Pro Ser
1315 1320 1325

Tyr Leu Asn Asn His Glu Arg Ser Ser Glu Gln Asn Arg Asn Met Met
1330 1335 1340

Asn Lys Leu Val Asp Asn Leu Gly Ser Gly Ser Glu Asp Asp Ala Ile
1345 1350 1355 1360

Val Leu Asp Asp Ala Ala Ser Phe Asn His Glu Glu Ser Leu Gly Leu
1365 1370 1375

Glu Leu Ile His Glu Glu Ser Asp Ala Pro Leu Leu Pro Pro Arg Val
1380 1385 1390

Tyr Ser Thr Asp Asn His Gln Pro His His Tyr Ser Arg Arg Arg Leu
1395 1400 1405

Pro Gln Asp His Ser Glu Ser Phe Phe Pro Leu Leu Thr Asp Glu His
1410 1415 1420

Thr Glu Asp Pro Gln Ser Pro His Arg Asp Ser Leu Tyr Thr Ser Met
1425 1430 1435 1440

Pro Ala Leu Ala Gly Val Pro Ala Ala Asp Ser Val Thr Thr Ser Thr
1445 1450 1455

Gln Thr Glu Ala Ala Ala Ala Lys Gly Gly Asp Ala Glu Asp Val Tyr
1460 1465 1470

Tyr Lys Ser Met Pro Asn Leu Gly Ser Arg Asn His Val His Pro Leu
1475 1480 1485

His Ala Tyr Tyr Gln Leu Gly Arg Gly Ser Ser Asp Gly Phe Ile Val
1490 1495 1500

Pro Pro Asn Lys Asp Gly Ala Ser Pro Glu Gly Thr Ser Lys Gly Pro
1505 1510 1515 1520

Ala His Leu Val Thr Ser Leu

1525

<210> 10
<211> 541
<212> PRT
<213> HUMAN

<400> 10

```
Met Asp Phe Glu Ser Gly Gln Val Asp Pro Leu Ala Ser Val Ile Leu
  1               5                  10                  15

Pro Pro Asn Leu Leu Glu Asn Leu Ser Pro Glu Asp Ser Val Leu Val
            20                  25                  30

Arg Arg Ala Gln Phe Thr Phe Phe Asn Lys Thr Gly Leu Phe Gln Asp
        35                  40                  45

Val Gly Pro Gln Arg Lys Thr Leu Val Ser Tyr Val Met Ala Cys Ser
    50                  55                  60

Ile Gly Asn Ile Thr Ile Gln Asn Leu Lys Asp Pro Val Gln Ile Lys
65                  70                  75                  80

Ile Lys His Thr Arg Thr Gln Glu Val His His Pro Ile Cys Ala Phe
                85                  90                  95

Trp Asp Leu Asn Lys Asn Lys Ser Phe Gly Gly Trp Asn Thr Ser Gly
            100                 105                 110

Cys Val Ala His Arg Asp Ser Asp Ala Ser Glu Thr Val Cys Leu Cys
        115                 120                 125

Asn His Phe Thr His Phe Gly Val Leu Met Asp Leu Pro Arg Ser Ala
    130                 135                 140

Ser Gln Leu Asp Ala Arg Asn Thr Lys Val Leu Thr Phe Ile Ser Tyr
145                 150                 155                 160

Ile Gly Cys Gly Ile Ser Ala Ile Phe Ser Ala Ala Thr Leu Leu Thr
                165                 170                 175

Tyr Val Ala Phe Glu Lys Leu Arg Arg Asp Tyr Pro Ser Lys Ile Leu
            180                 185                 190

Met Asn Leu Ser Thr Ala Leu Leu Phe Leu Asn Leu Leu Phe Leu Leu
        195                 200                 205
```

```
Asp Gly Trp Ile Thr Ser Phe Asn Val Asp Gly Leu Cys Ile Ala Val
    210                 215                 220

Ala Val Leu Leu His Phe Phe Leu Leu Ala Thr Phe Thr Trp Met Gly
225                 230                 235                 240

Leu Glu Ala Ile His Met Tyr Ile Ala Leu Val Lys Val Phe Asn Thr
                245                 250                 255

Tyr Ile Arg Arg Tyr Ile Leu Lys Phe Cys Ile Ile Gly Trp Gly Leu
            260                 265                 270

Pro Ala Leu Val Val Ser Val Val Leu Ala Ser Arg Asn Asn Asn Glu
        275                 280                 285

Val Tyr Gly Lys Glu Ser Tyr Gly Lys Glu Lys Gly Asp Glu Phe Cys
    290                 295                 300

Trp Ile Gln Asp Pro Val Ile Phe Tyr Val Thr Cys Ala Gly Tyr Phe
305                 310                 315                 320

Gly Val Met Phe Phe Leu Asn Ile Ala Met Phe Ile Val Val Met Val
                325                 330                 335

Gln Ile Cys Gly Arg Asn Gly Lys Arg Ser Asn Arg Thr Leu Arg Glu
            340                 345                 350

Glu Val Leu Arg Asn Leu Arg Ser Val Val Ser Leu Thr Phe Leu Leu
        355                 360                 365

Gly Met Thr Trp Gly Phe Ala Phe Phe Ala Trp Gly Pro Leu Asn Ile
    370                 375                 380

Pro Phe Met Tyr Leu Phe Ser Ile Phe Asn Ser Leu Gln Gly Leu Phe
385                 390                 395                 400

Ile Phe Ile Phe His Cys Ala Met Lys Glu Asn Val Gln Lys Gln Trp
                405                 410                 415

Arg Gln His Leu Cys Cys Gly Arg Phe Arg Leu Ala Asp Asn Ser Asp
            420                 425                 430

Trp Ser Lys Thr Ala Thr Asn Ile Ile Lys Lys Ser Ser Asp Asn Leu
        435                 440                 445

Gly Lys Ser Leu Ser Ser Ser Ser Ile Gly Ser Asn Ser Thr Tyr Leu
    450                 455                 460
```

```
Thr Ser Lys Ser Lys Ser Ser Ser Thr Thr Tyr Phe Lys Arg Asn Ser
465                 470                 475                 480

His Thr Asp Ser Ala Ser Met Asp Lys Ser Leu Ser Lys Leu Ala His
                485                 490                 495

Ala Asp Gly Asp Gln Thr Ser Ile Ile Pro Val His Gln Val Ile Asp
            500                 505                 510

Lys Val Lys Gly Tyr Cys Asn Ala His Ser Asp Asn Phe Tyr Lys Asn
        515                 520                 525

Ile Ile Met Ser Asp Thr Phe Ser His Ser Thr Lys Phe
    530                 535                 540
```

<210> 11
<211> 1582
<212> PRT
<213> Caenorhabditis elegans

<400> 11

```
Met Ala Thr Ala Ser Thr Glu Ile Ser Glu Phe Ser Glu Ala Ile Glu
  1               5                  10                  15

Ser Thr Phe Asp Leu Asp Phe Thr Ala His Gln Thr Glu Ile Ile Gly
            20                  25                  30

Thr Tyr Trp Asn Leu Arg Ala Leu Leu Arg Leu His Arg Ser Leu Val
        35                  40                  45

Ala Ile Asp His Val Ser Gln Lys Ser Phe Trp Glu Arg Tyr Asn His
    50                  55                  60

Trp Ile Gln Leu Ser Met Leu Val Ser Asn Gln Asn Val Asn Leu Cys
65                  70                  75                  80

Gln Ser Asn Ile Cys Gln Asn Gly Gly Thr Cys Leu Val Ala Ser Ser
                85                  90                  95

Val Pro Ala Thr Ala Thr Cys Pro Lys Asn Ser Ile Tyr Tyr Met Gly
            100                 105                 110

Ser Cys Tyr Val Phe Asp Thr Thr Leu Arg Asn Trp Asn Asp Ala Ala
        115                 120                 125

Leu Tyr Cys Asn Asn Met Asn Ser Ala Thr Leu Pro Leu Val Glu Ser
    130                 135                 140
```

```
Ala Glu Asp Gln Ala Phe Phe Ala Gly Tyr Leu Gln Ala Met Ile Pro
145                 150                 155                 160

Ser Asn Pro Pro Ala Asp Met Arg Pro Pro Pro Asp Gly Ile Trp Thr
                165                 170                 175

Ala Val Arg Gly Val Asn Asn Val Thr Arg Ala Ser Trp Val Tyr Tyr
            180                 185                 190

Pro Gly Ser Phe Leu Val Thr Asp Thr Phe Trp Ala Pro Gln Glu Pro
        195                 200                 205

Asn Ile Tyr Val Asn Tyr Asn Asp Val Cys Val Ala Leu Gln Ser Asp
    210                 215                 220

Ser Phe Tyr Arg Glu Trp Thr Thr Ala Leu Cys Thr Ile Leu Lys Tyr
225                 230                 235                 240

Thr Val Cys Lys Val Ala Pro Thr Gln Ile Gln Ala Lys Tyr Val Ala
                245                 250                 255

Gln Cys Ser Cys Pro Asn Gly Tyr Gly Gly Gln Thr Cys Glu Thr Gln
            260                 265                 270

Ser Thr Thr Asn Gln Gln Ala Ser Thr Gln Arg Thr Cys Gly Ser Asn
        275                 280                 285

Asp Phe Gln Phe Ser Cys Pro Asn Asp Gln Thr Ile Thr Val Asp Phe
    290                 295                 300

Ala Ser Phe Gly Ala Gln Gly Gly Ser Ile Ile Thr Ser Pro Pro Asp
305                 310                 315                 320

Ala Leu Leu Gln Gln Ile Val Gln Lys Val Asn Ala Glu Thr Lys Lys
                325                 330                 335

Thr Val Asn Phe Trp Ile Gly Thr Pro Asn Asn Cys Gln Leu Leu Met
            340                 345                 350

Val Thr Gly Ser Ser Thr Ser Tyr Ser Gln Cys Pro Ser Ser Pro Ser
        355                 360                 365

Ser Thr Ala Asn Val Ile Cys Ser Thr Val Pro Gln Ser Thr Ala Ser
    370                 375                 380

Val Ser Ala Arg Pro Thr Gln Ser Ala Pro Val Asp Pro Val Ser Gln
385                 390                 395                 400
```

```
Thr Met Ala Arg Arg Glu Val Tyr Thr Gly Val Gln Pro Ile Ala Ser
                405                 410                 415

Ala Leu Gly Gly Gln Ser Lys Lys Thr Asn Arg Lys Leu Asn Asn Ile
            420                 425                 430

Cys Gln Thr Lys Ile Gly Ala Pro Leu Ser Leu Phe Leu Phe Ser Arg
        435                 440                 445

Asn Glu Val Ile Thr Gly Phe Val Cys Ile Ser Leu Ile Ser Ala Ser
    450                 455                 460

Pro Gln Ile Ile Tyr Tyr Leu Cys Ala Val Ser Leu Ile Cys His Pro
465                 470                 475                 480

Ser Val Pro Asp Ser Ile Asn Lys Pro Arg Tyr Cys Lys Lys Glu Lys
                485                 490                 495

Lys Asp Gly Ile Thr Tyr Glu Gln Thr Arg Ala Cys Met Leu His Glu
            500                 505                 510

Gln Pro Cys Pro Asp Pro Gln Asn Val Glu Gly Thr Val Thr Arg Tyr
        515                 520                 525

Cys Asn Cys Gln Thr Ala Lys Trp Glu Thr Pro Asp Thr Thr Asn Cys
    530                 535                 540

Thr His Arg Trp Val Ala Glu Met Glu Thr Ala Ile Lys Asp Asn Gln
545                 550                 555                 560

Pro Val Glu Asp Ile Ser Ser Thr Val Asn Arg Gln Leu Lys Ser Thr
                565                 570                 575

Ile Glu Arg Thr Leu Phe Gly Gly Asp Ile Thr Gly Thr Val Arg Leu
            580                 585                 590

Ser Asn Asp Met Leu Ser Leu Ala Arg Asn Gln Phe Ser Val Leu Asn
        595                 600                 605

Asp Arg Asn Leu Arg Glu Asn Lys Ala Arg Asn Phe Thr Glu Asn Leu
    610                 615                 620

Gly Gly Ser Gly Asp Gln Leu Leu Ser Pro Val Ala Ala Thr Val Trp
625                 630                 635                 640

Asp Gln Leu Ser Ser Thr Ile Arg Ile Gln His Ala Ser Lys Leu Met
                645                 650                 655
```

```
Ser Val Leu Glu Gln Ser Val Leu Leu Leu Gly Asp Tyr Met Thr Asp
            660                 665                 670

Gln Lys Leu Asn Leu Gln Tyr Ile Asn Trp Ala Met Glu Val Glu Arg
        675                 680                 685

Ser Glu Pro Glu Val Gln Thr Phe Gly Ala Ala Ala Ser Pro Asn Val
    690                 695                 700

Gln Asp Asp Met Gly Met Met Arg Val Met Ala Ala Ala Pro Pro Ala
705                 710                 715                 720

Pro Gln Pro Glu Thr Asn Thr Thr Ile Met Phe Pro Ser Leu Lys Leu
                725                 730                 735

Ser Pro Thr Ile Thr Leu Pro Ser Ala Ser Leu Leu Ser Ser Leu Ala
            740                 745                 750

Ser Pro Thr Pro Val Ala Gly Gly Gly Pro Ser Ile Leu Ser Ser Phe
        755                 760                 765

Gln Asp Asp Thr Pro Val Gly Met Ala Ser Thr Pro Asn Leu Asn Arg
    770                 775                 780

Asn Pro Val Lys Leu Gly Tyr Tyr Ala Phe Ala Gly Phe Gly Gln Leu
785                 790                 795                 800

Leu Asn Asn Asn Asn Asp His Thr Leu Ile Asn Ser Gln Val Ile Gly
                805                 810                 815

Ala Ser Ile Gln Asn Ala Thr Gln Ser Val Thr Leu Pro Val Asp His
            820                 825                 830

Pro Val Thr Phe Thr Phe Gln His Leu Thr Thr Lys Gly Val Ser Asn
        835                 840                 845

Pro Arg Cys Val Tyr Trp Asp Leu Met Glu Ser Lys Trp Ser Thr Leu
    850                 855                 860

Gly Cys Thr Leu Ile Ala Thr Ser Ser Asn Ser Ser Gln Cys Ser Cys
865                 870                 875                 880

Thr His Leu Thr Ser Phe Ala Ile Leu Met Asp Ile Ser Gly Gln Val
                885                 890                 895

Gly Arg Leu Ser Gly Gly Leu Ala Ser Ala Leu Asp Val Val Ser Thr
            900                 905                 910
```

Ile Gly Cys Ala Ile Ser Ile Val Cys Leu Ala Leu Ser Val Cys Val
915 920 925

Phe Thr Phe Phe Arg Asn Leu Gln Asn Val Arg Asn Ser Ile His Arg
930 935 940

Asn Leu Cys Leu Cys Leu Leu Ile Ala Glu Leu Val Phe Val Ile Gly
945 950 955 960

Met Asp Arg Thr Gly Asn Arg Thr Gly Cys Gly Val Val Ala Ile Leu
965 970 975

Leu His Tyr Phe Phe Leu Ser Ser Phe Cys Trp Met Leu Leu Glu Gly
980 985 990

Tyr Gln Leu Tyr Met Met Leu Ile Gln Val Phe Glu Pro Asn Arg Thr
995 1000 1005

Arg Ile Phe Leu Tyr Tyr Leu Phe Cys Tyr Gly Thr Pro Ala Val Val
1010 1015 1020

Val Ala Ile Ser Ala Gly Ile Lys Trp Glu Asp Tyr Gly Thr Asp Ser
1025 1030 1035 1040

Tyr Cys Trp Ile Asp Thr Ser Thr Pro Thr Ile Trp Ala Phe Val Ala
1045 1050 1055

Pro Ile Ile Val Ile Ile Ala Ala Asn Ile Ile Phe Leu Leu Ile Ala
1060 1065 1070

Leu Lys Val Val Leu Ser Val Gln Ser Arg Asp Arg Thr Lys Trp Gly
1075 1080 1085

Arg Ile Ile Gly Trp Leu Lys Gly Ser Ala Thr Leu Leu Cys Leu Leu
1090 1095 1100

Gly Ile Thr Trp Ile Phe Gly Phe Leu Thr Ala Val Lys Gly Gly Thr
1105 1110 1115 1120

Gly Thr Ala Phe Ala Trp Ile Phe Thr Ile Leu Asn Cys Thr Gln Gly
1125 1130 1135

Ile Phe Ile Phe Val Leu His Val Val Leu Asn Glu Lys Val Arg Ala
1140 1145 1150

Ser Ile Val Arg Trp Leu Arg Thr Gly Ile Cys Cys Leu Pro Glu Thr
1155 1160 1165

Ser Ser Ala Ala Tyr Asn Ser Arg Ser Phe Leu Ser Ser Arg Gln Arg
1170 1175 1180

Ile Leu Asn Met Ile Lys Val Asn Gly His Ser Tyr Pro Ser Thr Ala
1185 1190 1195 1200

Ser Thr Asp Asp Lys Glu Lys Gln Leu Thr Pro Ile Thr Lys Thr Thr
1205 1210 1215

Asp Trp Leu Ser Arg Leu Pro Asn Gln Asp Ser Val Ser Ile Pro Glu
1220 1225 1230

Ser Asn Phe Asn Asn Leu Asn Gly Thr Leu Glu Asn Ser Asn Leu Asn
1235 1240 1245

Ser Ala Glu Ile Lys Glu Glu Asp Glu Ile Pro Glu Leu Arg Arg Arg
1250 1255 1260

Val Thr Val Asp Leu Asn Pro Met Ile Val Ser Asn Asn Glu Ile Glu
1265 1270 1275 1280

Arg Met Ser His Ala Ser Ser Asp Pro Arg Gly Ser Gln Ile Ile Glu
1285 1290 1295

Val Thr Ala Val Glu Lys Lys Ala Pro Val Lys Arg Ile Lys Phe Pro
1300 1305 1310

Leu Gly Ala Lys Gln Ser Glu Arg Gly Ser Gln His Arg Thr Lys Ala
1315 1320 1325

Lys His Gly Thr Gly Thr Leu Val Ser Pro Trp His Ile Val Thr Ala
1330 1335 1340

Ala His Leu Ile Gly Ile Ser Glu Asp Pro Leu Pro Asp Cys Asp Thr
1345 1350 1355 1360

Gly Asn Leu Arg Glu Ala Tyr Phe Val Arg Asp Tyr Lys Asn Phe Val
1365 1370 1375

Ala Phe Val Asn Val Thr Cys Ala Val Pro Glu Met Cys Lys Gly Leu
1380 1385 1390

His Arg Lys Asp Met Phe Lys Pro Leu Ala Ile Lys Ser Leu Tyr Ile
1395 1400 1405

Arg Lys Gly Tyr Val Gly Asp Gly Cys Ile Asp Arg Glu Ser Phe Asn
1410 1415 1420

```
Asp Ile Ala Val Phe Glu Leu Glu Glu Pro Ile Glu Phe Ser Lys Asp
1425                1430                1435                1440

Ile Phe Pro Ala Cys Leu Pro Ser Ala Pro Lys Ile Pro Arg Ile Arg
                1445                1450                1455

Glu Thr Gly Tyr Lys Leu Phe Gly Tyr Gly Arg Asp Pro Ser Asp Ser
            1460                1465                1470

Val Leu Glu Ser Gly Lys Leu Lys Ser Leu Tyr Ser Phe Val Ala Glu
        1475                1480                1485

Cys Ser Asp Asp Phe Pro Tyr Gly Gly Val Tyr Cys Thr Ser Ala Val
    1490                1495                1500

Asn Arg Gly Leu Ser Cys Asp Gly Asp Ser Gly Ser Gly Val Val Arg
1505                1510                1515                1520

Thr Ser Asp Thr Arg Asn Val Gln Val Leu Val Gly Val Leu Ser Ala
                1525                1530                1535

Gly Met Pro Cys Pro Glu Leu Tyr Asp Thr His Asn Arg Gln Arg Gln
            1540                1545                1550

Gln Arg Arg Gln Leu Thr Gln Glu Thr Asp Leu Leu Val Asp Val Ser
        1555                1560                1565

Ala His Val Asp Phe Phe Cys Thr Cys Cys Gly Met Cys Ser
    1570                1575                1580


<210> 12
<211> 198
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
      peptide

<400> 12
Met Glu Thr Tyr Ser Leu Ser Leu Gly Asn Gln Ser Val Val Glu Pro
  1               5                  10                  15

Asn Ile Ala Ile Gln Ser Ala Asn Phe Ser Ser Glu Asn Ala Val Gly
             20                  25                  30
```

```
Pro Ser Asn Val Arg Phe Ser Val Gln Lys Gly Ala Ser Ser Ser Leu
         35                  40                  45

Val Ser Ser Ser Thr Phe Ile His Thr Asn Val Asp Gly Leu Asn Pro
     50                  55                  60

Asp Ala Gln Thr Glu Leu Gln Val Leu Leu Asn Met Thr Lys Asn Tyr
 65                  70                  75                  80

Thr Lys Thr Cys Gly Phe Val Val Tyr Gln Asn Asp Lys Leu Phe Gln
                 85                  90                  95

Ser Lys Thr Phe Thr Ala Lys Ser Asp Phe Ser Gln Lys Ile Ile Ser
            100                 105                 110

Ser Lys Thr Asp Glu Asn Glu Gln Asp Gln Ser Ala Ser Val Asp Met
        115                 120                 125

Val Phe Ser Pro Lys Tyr Asn Gln Lys Glu Phe Gln Leu Tyr Ser Tyr
    130                 135                 140

Ala Cys Val Tyr Trp Asn Leu Ser Ala Lys Asp Trp Asp Thr Tyr Gly
145                 150                 155                 160

Cys Gln Lys Asp Lys Gly Thr Asp Gly Phe Leu Arg Cys Arg Cys Asn
                165                 170                 175

His Thr Thr Asn Phe Ala Val Leu Met Thr Phe Lys Lys Asp Tyr Gln
            180                 185                 190

Tyr Pro Lys Ser Leu Asp
        195
```

<210> 13
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized peptide

<400> 13
```
Gln Ile Val Thr Arg Lys Val Arg Lys Thr
  1               5                  10
```

<210> 14
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized peptide

<400> 14
Glu Asn Ser Asn Lys Asn Leu Gln Thr Ser Asp Gly Asp Ile Asn Asn
1 5 10 15

Ile Asp Phe Asp Asn Asn Asp Ile Pro Arg Thr Asp Thr Ile Asn Ile
20 25 30

Pro Asn Pro Met Cys Thr
35

<210> 15
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized peptide

<400> 15
Ile Arg Thr Met Lys Pro Leu Pro Arg His
1 5 10

<210> 16
<211> 41
<212> PRT
<213> Artificial Sequence

<400> 16
Thr Val Gly Val Ile Tyr Ser Gln Asn Gly Asn Asn Pro Gln Trp Glu
1 5 10 15

Leu Asp Tyr Arg Gln Glu Lys Ile Cys Trp Leu Ala Ile Pro Glu Pro
20 25 30

Asn Gly Val Ile Lys Ser Pro Leu Leu
35 40

<210> 17
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized peptide

<400> 17
Thr Ile Ser Ile Lys Val Leu Trp Lys Asn Asn Gln Asn Leu Thr Ser
1 5 10 15

Thr Lys Lys Val Ser Ser Met Lys Lys
20 25

<210> 18
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized peptide

<400> 18
Asn Asp Asp Ser Ile Arg
1 5

<210> 19
<211> 78
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized peptide

<400> 19
Tyr Thr Val Arg Thr Lys Val Phe Gln Ser Glu Ala Ser Lys Val Leu
1 5 10 15

Met Leu Leu Ser Ser Ile Gly Arg Arg Lys Ser Leu Pro Ser Val Thr
20 25 30

Arg Pro Arg Leu Arg Val Lys Met Tyr Asn Phe Leu Arg Ser Leu Pro
35 40 45

Thr Leu His Glu Arg Phe Arg Leu Leu Glu Thr Ser Pro Ser Thr Glu
50 55 60

Glu Ile Thr Leu Ser Glu Ser Asp Asn Ala Lys Glu Ser Ile
65 70 75

<210> 20
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: HGPRBMY6 5'
PRIMER

<400> 20
cgggatgcct agatgctttc ctttgcattg tcactttc 38

<210> 21
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: HGPRBMY6 3'
FLAG TAG PRIMER

<400> 21
cggggatccc tacttgtcgt cgtcgtcctt gtagtccatg atgctttcct ttgcattgtc 60
actttc 66

<210> 22
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: HGPRBMY6
Forward primer 383

<400> 22

cagacaccat taacatcccg aat 23

<210> 23
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: HGPRBMY6
Reverse primer 384

<400> 23
agaatgaaat gccgaggaag ag 22

<210> 24
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: GAPDH-F3
forward primer

<400> 24
agccgagcca catcgct 17

<210> 25
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: GAPDH-R1
reverse primer

<400> 25
gtgaccaggc gcccaatac 19

<210> 26
<211> 28
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: GAPDH-PVIC
Taqman(R) Probe

<400> 26
caaatccgtt gactccgacc ttcacctt 28

<210> 27
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 27
Gln Ser Lys Thr Phe Thr Ala Lys Ser Asp Phe Ser Gln
1 5 10

<210> 28
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 28
Ala Lys Ser Asp Phe Ser Gln Lys Ile Ile Ser Ser Lys
1 5 10

<210> 29
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 29
Ser Gln Lys Ile Ile Ser Ser Lys Thr Asp Glu Asn Glu
1 5 10

<210> 30
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 30
Val Asp Met Val Phe Ser Pro Lys Tyr Asn Gln Lys Glu
1 5 10

<210> 31
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 31
Val Tyr Trp Asn Leu Ser Ala Lys Asp Trp Asp Thr Tyr
1 5 10

<210> 32
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 32
Phe Ala Val Leu Met Thr Phe Lys Lys Asp Tyr Gln Tyr
1 5 10

<210> 33
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 33
Ile Phe Gln Ile Val Thr Arg Lys Val Arg Lys Thr Ser
1 5 10

<210> 34
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 34
Phe Gly Ile Glu Asn Ser Asn Lys Asn Leu Gln Thr Ser
1 5 10

<210> 35
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 35
Tyr Leu Leu Ile Arg Thr Met Lys Pro Leu Pro Arg His
1 5 10

<210> 36
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 36
Met Phe Ile Thr Ile Ser Ile Lys Val Leu Trp Lys Asn

1 5 10

<210> 37
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 37
Asn Gln Asn Leu Thr Ser Thr Lys Lys Val Ser Ser Met
1 5 10

<210> 38
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 38
Gln Asn Leu Thr Ser Thr Lys Lys Val Ser Ser Met Lys
1 5 10

<210> 39
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 39
Thr Lys Lys Val Ser Ser Met Lys Lys Ile Val Ser Thr
1 5 10

<210> 40
<211> 13
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 40
Leu Val Asn Asp Asp Ser Ile Arg Ile Val Phe Ser Tyr
1 5 10

<210> 41
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 41
Ile Phe Ile Leu Tyr Thr Val Arg Thr Lys Val Phe Gln
1 5 10

<210> 42
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 42
Ser Leu Gly Asn Gln Ser Val Val Glu Pro Asn Ile Ala Ile
1 5 10

<210> 43
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 43
Ser Thr Phe Ile His Thr Asn Val Asp Gly Leu Asn Pro Asp
1 5 10

<210> 44
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 44
Gln Lys Ile Ile Ser Ser Lys Thr Asp Glu Asn Glu Gln Asp
1 5 10

<210> 45
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 45
Val Tyr Trp Asn Leu Ser Ala Lys Asp Trp Asp Thr Tyr Gly
1 5 10

<210> 46
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 46
Lys Asn Leu Gln Thr Ser Asp Gly Asp Ile Asn Asn Ile Asp
1 5 10

<210> 47

<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 47
Leu Arg Ser Leu Pro Thr Leu His Glu Arg Phe Arg Leu Leu
1 5 10

<210> 48
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 48
Leu Glu Thr Ser Pro Ser Thr Glu Glu Ile Thr Leu Ser Glu
1 5 10

<210> 49
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 49
Ser Thr Glu Glu Ile Thr Leu Ser Glu Ser Asp Asn Ala Lys
1 5 10

<210> 50
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

polypeptide

<400> 50
Glu Glu Ile Thr Leu Ser Glu Ser Asp Asn Ala Lys Glu Ser
1 5 10

<210> 51
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 51
Val Thr Arg Lys Val Arg Lys Thr Ser Val Thr Trp Val Leu
1 5 10

<210> 52
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 52
Asn Leu Thr Ser Thr Lys Lys Val Ser Ser Met Lys Lys Ile
1 5 10

<210> 53
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 53
Leu Ser Ser Ile Gly Arg Arg Lys Ser Leu Pro Ser Val Thr
1 5 10

<210> 54
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 54
Ser Leu Ser Leu Gly Asn Gln Ser Val Val Glu Pro Asn Ile
1 5 10

<210> 55
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 55
Ala Ile Gln Ser Ala Asn Phe Ser Ser Glu Asn Ala Val Gly
1 5 10

<210> 56
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 56
Leu Gln Val Leu Leu Asn Met Thr Lys Asn Tyr Thr Lys Thr
1 5 10

<210> 57
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 57
Leu Asn Met Thr Lys Asn Tyr Thr Lys Thr Cys Gly Phe Val
1 5 10

<210> 58
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 58
Ala Cys Val Tyr Trp Asn Leu Ser Ala Lys Asp Trp Asp Thr
1 5 10

<210> 59
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 59
Leu Arg Cys Arg Cys Asn His Thr Thr Asn Phe Ala Val Leu
1 5 10

<210> 60
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 60
Trp Lys Asn Asn Gln Asn Leu Thr Ser Thr Lys Lys Val Ser

1 5 10

<210> 61
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 61
Ile Phe Cys Leu Phe Asn Thr Thr Gln Gly Leu Gln Ile Phe
1 5 10

<210> 62
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 62
Phe Ser Val Gln Lys Gly Ala Ser Ser Ser Leu Val Ser Ser Ser Thr
1 5 10 15

<210> 63
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 63
Ile Leu Ser Asn Val Gly Cys Ala Leu Ser Val Thr Gly Leu Ala Leu
1 5 10 15

<210> 64
<211> 16
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 64
Ala Leu Ser Val Thr Gly Leu Ala Leu Thr Val Ile Phe Gln Ile Val
1 5 10 15

<210> 65
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 65
Leu Leu Phe Val Phe Gly Ile Glu Asn Ser Asn Lys Asn Leu Gln Thr
1 5 10 15

<210> 66
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 66
Val Ala Ile Thr Val Gly Val Ile Tyr Ser Gln Asn Gly Asn Asn Pro
1 5 10 15

<210> 67
<211> 99
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligo 1;
N=A+G+C+T; K=C+G+T

<400> 67
cgaagcgtaa gggcccagcc ggccnnknnk nnknnknnkn nknnknnknn knnknnknnk 60
nnknnknnkn nknnknnknn knnkccgggt ccgggcggc 99

<210> 68
<211> 98
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligo 2;
N=A+G+C+T; V=C+A+G

<400> 68
aaaaggaaaa aagcggccgc vnnvnnvnnv nnvnnvnnvn nvnnvnnvnn vnnvnnvnnv 60
nnvnnvnnvn nvnnvnnvnn vnngccgccc ggacccgg 98

<210> 69
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 69
Pro Gly Pro Gly Gly
1 5

<210> 70
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 70
Phe Ala Gly Gln Ile Ile Trp Tyr Asp Ala Leu Asp Thr Leu Met
1 5 10 15

<210> 71

<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 71
Ser Asp Phe Val Gly Gly Phe Trp Phe Trp Asp Ser Leu Phe Asn
1 5 10 15

<210> 72
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 72
Gly Asp Phe Trp Tyr Glu Ala Cys Glu Ser Ser Cys Ala Phe Trp
1 5 10 15

<210> 73
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 73
Leu Glu Trp Gly Ser Asp Val Phe Tyr Asp Val Tyr Asp Cys Cys
1 5 10 15

<210> 74
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

polypeptide

<400> 74
Arg Ile Asp Ser Cys Ala Lys Tyr Phe Leu Arg Ser Cys Asp
1 5 10

<210> 75
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 75
Cys Leu Arg Ser Gly Thr Gly Cys Ala Phe Gln Leu Tyr Arg Phe
1 5 10 15

<210> 76
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 76
Phe Arg Val Ser Arg Val Trp Asn Pro Pro Ser Phe Asp Ser Ala
1 5 10 15

<210> 77
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 77
His Ala Tyr Val Glu Cys Asn Asp Thr Asp Cys Arg Val Trp Phe
1 5 10 15

<210> 78
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic 5' Primer

<400> 78
gcagcagcgg ccgcgacata ttatccaacg ttggatgtg 39

<210> 79
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic 3' Primer

<400> 79
gcagcagtcg acgatgcttt cctttgcatt gtcac 35

<210> 80
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic 5' Primer

<400> 80
gcagcagcgg ccgcatggag acttattcct tgtctttgg 39

<210> 81
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic 3' Primer

<400> 81
gcagcagtcg acgtacagga taaaaatttg caatccc 37